



## Prevalence of rare mitochondrial DNA mutations in mitochondrial disorders

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Résumé en  
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**BACKGROUND:** Mitochondrial DNA (mtDNA) diseases are rare disorders whose prevalence is estimated around 1 in 5000. Patients are usually tested only for deletions and for common mutations of mtDNA which account for 5-40% of cases, depending on the study. However, the prevalence of rare mtDNA mutations is not known. **METHODS:** We analysed the whole mtDNA in a cohort of 743 patients suspected of manifesting a mitochondrial disease, after excluding deletions and common mutations. Both heteroplasmic and homoplasmic variants were identified using two complementary strategies (Surveyor and MitoChip). Multiple correspondence analyses followed by hierarchical ascendant cluster process were used to explore relationships between clinical spectrum, age at onset and localisation of mutations. **RESULTS:** 7.4% of deleterious mutations and 22.4% of novel putative mutations were identified. Pathogenic heteroplasmic mutations were more frequent than homoplasmic mutations (4.6% vs 2.8%). Patients carrying deleterious mutations showed symptoms before 16 years of age in 67% of cases. Early onset disease (<1 year) was significantly associated with mutations in protein coding genes (mainly in complex I) while late onset disorders (>16 years) were associated with mutations in tRNA genes. MTND5 and MTND6 genes were identified as 'hotspots' of mutations, with Leigh syndrome accounting for the large majority of associated phenotypes. **CONCLUSIONS:** Rare mitochondrial DNA mutations probably account for more than 7.4% of patients with respiratory chain deficiency. This study shows that a comprehensive analysis of mtDNA is essential, and should include young children, for an accurate diagnosis that is now accessible with the development of next generation sequencing technology.

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